

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Pelleymounter, Mary Ann  
Hecht, Randy I  
Mann, Michael B
- (ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Amgen Inc.
  - (B) STREET: 1840 Dehavilland Drive
  - (C) CITY: Thousand Oaks
  - (D) STATE: California
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 91230-1789
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/474,833
  - (B) FILING DATE: 07-JUN-1995
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Pessin, Karol M.
  - (C) REFERENCE/DOCKET NUMBER: A-345

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 491 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT	60
TCAGGACGAC ACCAAAACCT TAATTAAAC GATCGTTACG CGTATCAACG ACATCAGTCA	120
CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA	180
CCCGATCCTA AGCTTGTTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC	240
CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT	300
GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA	360

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ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT 420  
 GTCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG 480  
 TTAATGGATC C 491

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTAAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA 60  
 AGTCCTGCTG TGGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TG TAGTCAGT 120  
 GTGGGTCAGC CAGAGGCGAT TTGTCGCACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT 180  
 GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG 240  
 GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA 300  
 CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT 360  
 TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAAACGAGA 420  
 CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC 480  
 AATTACCTAG G 491

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 147 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys  
 1 5 10 15  
 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser  
 20 25 30  
 Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro  
 35 40 45  
 Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln

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50		55		60											
Val 65	Leu 66	Thr 67	Ser 68	Leu 69	Pro 70	Ser 71	Gln 72	Asn 73	Val 74	Leu 75	Gln 76	Ile 77	Ala 78	Asn 79	Asp 80
Leu 81	Glu 82	Asn 83	Leu 84	Arg 85	Asp 86	Leu 87	Leu 88	His 89	Leu 90	Leu 91	Ala 92	Phe 93	Ser 94	Lys 95	Ser 96
Cys 97	Ser 98	Leu 99	Pro 100	Gln 101	Thr 102	Ser 103	Gly 104	Leu 105	Gln 106	Lys 107	Pro 108	Glu 109	Ser 110	Leu 111	Asp 112
Gly 113	Val 114	Leu 115	Glu 116	Ala 117	Ser 118	Leu 119	Tyr 120	Ser 121	Thr 122	Glu 123	Val 124	Val 125	Ala 126	Leu 127	Ser 128
Arg 129	Leu 130	Gln 131	Gly 132	Ser 133	Leu 134	Gln 135	Asp 136	Ile 137	Leu 138	Gln 139	Gln 140	Leu 141	Asp 142	Val 143	Ser 144
Pro 145	Glu 146	Cys 147													

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATGGTAC	CGATCCAGAA	AGTTCAGGAC	GACACCAAAA	CCTTAATTAA	AACGATCGTT	60
ACGCGTATCA	ACGACATCAG	TCACACCCAG	TCGGTGAGCT	CTAAACAGCG	TGTTACAGGC	120
CTGGACTTCA	TCCCGGGTCT	GCACCCGATC	CTGACCTTGT	CCAAAATGGA	CCAGACCCTG	180
GCTGTATACC	AGCAGATCTT	AACCTCCATG	CCGTCCCGTA	ACGTTCTTCA	GATCTCTAAC	240
GACCTCGAGA	ACCTTCGCGA	CCTGCTGCAC	GTGCTGGCAT	TCTCCAAATC	CTGCCACCTG	300
CCATGGGCTT	CAGGTCTTGA	GACTCTGGAC	TCTCTGGGCG	GGGTCCTGGA	AGCATCCGGT	360
TACAGCACCG	AAGTTGTTGC	TCTGTCCCGT	CTGCAGGGTT	CCCTTCAGGA	CATGCTTTGG	420
CAGCTGGACC	TGTCTCCGGG	TTGTTAATGG	ATCC			454

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA      60
TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTTGTCGC ACAATGTCCG      120
GACCTGAAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC      180
CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG      240
CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC      300
GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA      360
ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAGTCCT GTACGAAACC      420
GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG                                     454

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## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
1           5           10           15
Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
20           25           30
Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
35           40           45
Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
50           55           60
Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
65           70           75           80
Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
85           90           95
Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
100          105          110
Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
115          120          125
Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
130          135          140
Pro Gly Cys
145

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